Amendments to the Specification:

Please replace paragraph bridging pages 10 and 11 with the following amended paragraph:

For example, in the mass spectrum of a 1425.7 Da peptide (HSDAVFTDNYTR (SEQ ID NO:1)) isolated in an MS/MS experiment acquired in positive ion mode, the difference between the full peptide 1425.7 Da and the next largest mass fragment (y_{11}, 1288.7 Da) is 137 Da. This corresponds to the expected mass of an N-terminal histidine residue that is cleaved at the amide bond. For this peptide, complete sequencing is possible as a result of the generation of high-abundance fragment ions that correspond to cleavage of the peptide at almost every residue along the peptide backbone. The generation of an essentially complete set of positively-charged fragment ions that include either end of the peptide is a result of the basicity of both the N- and C-terminal residues (H and R, respectively). If a basic residue is located at the N- or C-terminus, especially R, most of the ions produced in the CID spectrum will contain that residue since positive charge is essentially localized at that site. This greatly simplifies the resulting spectrum since these basic sites direct the fragmentation into a limited series of specific daughter ions. Peptides that lack basic residues tend to fragment into a more complex mixture of fragment ions that makes sequence determination more difficult.

Please replace the second paragraph on page 105 with the following amended paragraph:

The deduced N-terminal amino acid sequence of glycogen phosphorylase A from Example 1 (*i.e.*, SRPLSD (SEQ ID NO:2)) was used to search the SWIS-PROT and TrEMBEL protein sequence databases using the published ExPASy TagIdent tool (*see,* http://www.expasy.ch/tools/tagident.html). This tool enables searching known protein sequences contained within the database for any that contain matching sequences to a 1-6 continguous amino acid PST. The search can be limited by the position of the PST in the protein (*i.e.*, N-terminal or C-terminal) and the use of the electrophoretic coordinates isoelectric point and/or apparent molecular weight.

Please replace the second paragraph on page 106 with the following amended paragraph:

The deduced N-terminal amino acid sequence of bradykinin determined from Examples 2 and 3 (*i.e.*, RPPGFS (SEQ ID NO:5)) was used to search the SWIS-PROT and TrEMBEL protein sequence databases as described in Example 6.

Please replace the final paragraph on page 106 with the following amended paragraph:

Table 3

Human Bradykinin Identification from a

Genomic Database using an N-terminal IMLS PST

PST	Number of hits based on PST	Number of N-terminal hits	Number of N-terminal hits limited by MW
RP	4114	13	1
RPP	638	4	1
RPPG (SEQ ID NO: 3	66	1	1
RPPGF (SEQ ID NO:4	5	1	1
RPPGFS (SEQ ID NO: 5	3	1	1